

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LANG, Florian
WALDEGGER, Tübingen
- (ii) TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: FOLEY & LARDNER
(B) STREET: 3000 K Street, N.W.
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: U.S.A.
(F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/031,295
(B) FILING DATE: 26-FEB-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: DE 197-08-173.8
(B) FILING DATE: 28-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Sandercock, Colin G.
(B) REGISTRATION NUMBER: 31,298
(C) REFERENCE/DOCKET NUMBER: 058315/0123
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (202) 672-5300
(B) TELEFAX: (202) 672-5399

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 43..1335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACGAGGGGAG CGCTAACGTC TTTCTGTCTC CCCGCGGTGG TG ATG ACG GTG AAA	54
Met Thr Val Lys	
1	
ACT GAG GCT GCT AAG GGC ACC CTC ACT TAC TCC AGG ATG AGG GGC ATG	102
Thr Glu Ala Ala Lys Gly Thr Leu Thr Tyr Ser Arg Met Arg Gly Met	
5 10 15 20	
GTG GCA ATT CTC ATC GCT TTC ATG AAG CAG AGG AGG ATG GGT CTG AAC	150
Val Ala Ile Leu Ile Ala Phe Met Lys Gln Arg Arg Met Gly Leu Asn	
25 30 35	
GAC TTT ATT CAG AAG ATT GCC AAT AAC TCC TAT GCA TGC AAA CAC CCT	198
Asp Phe Ile Gln Lys Ile Ala Asn Asn Ser Tyr Ala Cys Lys His Pro	
40 45 50	
GAA GTT CAG TCC ATC TTG AAG ATC TCC CAA CCT CAG GAG CCT GAG CTT	246
Glu Val Gln Ser Ile Leu Lys Ile Ser Gln Pro Gln Glu Pro Glu Leu	
55 60 65	
ATG AAT GCC AAC CCT TCT CCT CCA CCA AGT CCT TCT CAG CAA ATC AAC	294
Met Asn Ala Asn Pro Ser Pro Pro Pro Ser Pro Ser Gln Gln Ile Asn	
70 75 80	
CTT GGC CCG TCG TCC AAT CCT CAT GCT AAA CCA TCT GAC TTT CAC TTC	342
Leu Gly Pro Ser Ser Asn Pro His Ala Lys Pro Ser Asp Phe His Phe	
85 90 95 100	
TTG AAA GTG ATC GGA AAG GGC AGT TTT GGA AAG GTT CTT CTA GCA AGA	390
Leu Lys Val Ile Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Ala Arg	
105 110 115	
CAC AAG GCA GAA GAA GTG TTC TAT GCA GTC AAA GTT TTA CAG AAG AAA	438
His Lys Ala Glu Val Phe Tyr Ala Val Lys Val Leu Gln Lys Lys	
120 125 130	
GCA ATC CTG AAA AAG AAA GAG GAG AAG CAT ATT ATG TCG GAG CGG AAT	486
Ala Ile Leu Lys Lys Lys Glu Glu Lys His Ile Met Ser Glu Arg Asn	
135 140 145	
GTT CTG TTG AAG AAT GTG AAG CAC CCT TTC CTG GTG GGC CTT CAC TTC	534
Val Leu Leu Lys Asn Val Lys His Pro Phe Leu Val Gly Leu His Phe	
150 155 160	
TCT TTC CAG ACT GCT GAC AAA TTG TAC TTT GTC CTA GAC TAC ATT AAT	582
Ser Phe Gln Thr Ala Asp Lys Leu Tyr Phe Val Leu Asp Tyr Ile Asn	
165 170 175 180	
GGT GGA GAG TTG TTC TAC CAT CTC CAG AGG GAA CGC TGC TTC CTG GAA	630
Gly Gly Glu Leu Phe Tyr His Leu Gln Arg Glu Arg Cys Phe Leu Glu	
185 190 195	
CCA CGG GCT CGT TTC TAT GCT GCT GAA ATA GCC AGT GCC TTG GGC TAC	678
Pro Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ala Ser Ala Leu Gly Tyr	
200 205 210	
CTG CAT TCA CTG AAC ATC GTT TAT AGA GAC TTA AAA CCA GAG AAT ATT	726
Leu His Ser Leu Asn Ile Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile	
215 220 225	

T04021 5E00000T

TTG CTA GAT TCA CAG GGA CAC ATT GTC CTT ACT GAT TTC GGA CTC TGC Leu Leu Asp Ser Gln Gly His Ile Val Leu Thr Asp Phe Gly Leu Cys 230 235 240	774
AAG GAG AAC ATT GAA CAC AAC AGC ACA ACA TCC ACC TTC TGT GGC ACG Lys Glu Asn Ile Glu His Asn Ser Thr Thr Ser Thr Phe Cys Gly Thr 245 250 255 260	822
CCG GAG TAT CTC GCA CCT GAG GTG CTT CAT AAG CAG CCT TAT GAC AGG Pro Glu Tyr Leu Ala Pro Glu Val Leu His Lys Gln Pro Tyr Asp Arg 265 270 275	870
ACT GTG GAC TGG TGG TGC CTG GGA GCT GTC TTG TAT GAG ATG CTG TAT Thr Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr Glu Met Leu Tyr 280 285 290	918
GGC CTG CCG CCT TTT TAT AGC CGA AAC ACA GCT GAA ATG TAC GAC AAC Gly Leu Pro Pro Phe Tyr Ser Arg Asn Thr Ala Glu Met Tyr Asp Asn 295 300 305	966
ATT CTG AAC AAG CCT CTC CAG CTG AAA CCA AAT ATT ACA AAT TCC GCA Ile Leu Asn Lys Pro Leu Gln Leu Lys Pro Asn Ile Thr Asn Ser Ala 310 315 320	1014
AGA CAC CTC CTG GAG GGC CTC CTG CAG AAG GAC AGG ACA AAG CGG CTC Arg His Leu Leu Glu Gly Leu Leu Gln Lys Asp Arg Thr Lys Arg Leu 325 330 335 340	1062
GGG GCC AAG GAT GAC TTC ATG GAG ATT AAG AGT CAT GTC TTC TTC TCC Gly Ala Lys Asp Asp Phe Met Glu Ile Lys Ser His Val Phe Phe Ser 345 350 355	1110
TTA ATT AAC TGG GAT GAT CTC ATT AAT AAG AAG ATT ACT CCC CCT TTT Leu Ile Asn Trp Asp Asp Leu Ile Asn Lys Lys Ile Thr Pro Pro Phe 360 365 370	1158
AAC CCA AAT GTG AGT GGG CCC AAC GAG CTA CGG CAC TTT GAC CCC GAG Asn Pro Asn Val Ser Gly Pro Asn Glu Leu Arg His Phe Asp Pro Glu 375 380 385	1206
TTT ACC GAA GAG CCT GTC CCC AAC TCC ATT GGC AAG TCC CCT GAC AGC Phe Thr Glu Glu Pro Val Pro Asn Ser Ile Gly Lys Ser Pro Asp Ser 390 395 400	1254
GTC CTC GTC ACA GCC AGC GTC AAG GAA GCT GCC GAG GCT TTC CTA GGC Val Leu Val Thr Ala Ser Val Lys Glu Ala Ala Glu Ala Phe Leu Gly 405 410 415 420	1302
TTT TCC TAT GCG CCT CCC ACG GAC TCT TTC CTC TGAACCCTGT TAGGGCTTGG Phe Ser Tyr Ala Pro Pro Thr Asp Ser Phe Leu 425 430	1355
TTTTAAAGGA TTTTATGTGT GTTTCGAAT GTTTTAGTTA GCCTTTTGGT GGAGCCGCCA	1415
GCTGACAGGA CATCTTACAA GAGAATTTGC ACATCTCTGG AAGCTTAGCA ATCTTATTGC	1475
ACACTGTTTCG CTGGAATTTT TTGAAGAGCA CATTCTCCTC AGTGAGCTCA TGAGGTTTTC	1535
ATTTTTATTTC TTCCTTCCAA CGTGGTGCTA TCTCTGAAAC GAGCGTTAGA GTGCCGCCTT	1595
AGACGGAGGC AGGAGTTTCG TTAGAAAGCG GACCTGTTCT AAAAAAGGTC TCCTGCAGAT	1655
CTGTCTGGGC TGTGATGACG AATATTATGA AATGTGCCTT TTCTGAAGAG ATTGTGTTAG	1715

T0402T 6E0000T

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 431 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met 1	Thr	Val	Lys	Thr 5	Glu	Ala	Ala	Lys	Gly 10	Thr	Leu	Thr	Tyr	Ser 15	Arg
Met	Arg	Gly	Met 20	Val	Ala	Ile	Leu	Ile 25	Ala	Phe	Met	Lys	Gln 30	Arg	Arg
Met	Gly	Leu 35	Asn	Asp	Phe	Ile	Gln 40	Lys	Ile	Ala	Asn	Asn 45	Ser	Tyr	Ala
Cys	Lys 50	His	Pro	Glu	Val	Gln 55	Ser	Ile	Leu	Lys	Ile 60	Ser	Gln	Pro	Gln
Glu 65	Pro	Glu	Leu	Met	Asn 70	Ala	Asn	Pro	Ser	Pro 75	Pro	Pro	Ser	Pro	Ser 80
Gln	Gln	Ile	Asn	Leu 85	Gly	Pro	Ser	Ser	Asn 90	Pro	His	Ala	Lys	Pro 95	Ser
Asp	Phe	His	Phe 100	Leu	Lys	Val	Ile	Gly 105	Lys	Gly	Ser	Phe	Gly 110	Lys	Val
Leu	Leu	Ala 115	Arg	His	Lys	Ala	Glu 120	Glu	Val	Phe	Tyr	Ala 125	Val	Lys	Val
Leu	Gln 130	Lys	Lys	Ala	Ile	Leu 135	Lys	Lys	Lys	Glu	Glu 140	Lys	His	Ile	Met

Ser Glu Arg Asn Val Leu Leu Lys Asn Val Lys His Pro Phe Leu Val
 145 150 155 160
 Gly Leu His Phe Ser Phe Gln Thr Ala Asp Lys Leu Tyr Phe Val Leu
 165 170 175
 Asp Tyr Ile Asn Gly Gly Glu Leu Phe Tyr His Leu Gln Arg Glu Arg
 180 185 190
 Cys Phe Leu Glu Pro Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ala Ser
 195 200 205
 Ala Leu Gly Tyr Leu His Ser Leu Asn Ile Val Tyr Arg Asp Leu Lys
 210 215 220
 Pro Glu Asn Ile Leu Leu Asp Ser Gln Gly His Ile Val Leu Thr Asp
 225 230 235 240
 Phe Gly Leu Cys Lys Glu Asn Ile Glu His Asn Ser Thr Thr Ser Thr
 245 250 255
 Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu His Lys Gln
 260 265 270
 Pro Tyr Asp Arg Thr Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr
 275 280 285
 Glu Met Leu Tyr Gly Leu Pro Pro Phe Tyr Ser Arg Asn Thr Ala Glu
 290 295 300
 Met Tyr Asp Asn Ile Leu Asn Lys Pro Leu Gln Leu Lys Pro Asn Ile
 305 310 315 320
 Thr Asn Ser Ala Arg His Leu Leu Glu Gly Leu Leu Gln Lys Asp Arg
 325 330 335
 Thr Lys Arg Leu Gly Ala Lys Asp Asp Phe Met Glu Ile Lys Ser His
 340 345 350
 Val Phe Phe Ser Leu Ile Asn Trp Asp Asp Leu Ile Asn Lys Lys Ile
 355 360 365
 Thr Pro Pro Phe Asn Pro Asn Val Ser Gly Pro Asn Glu Leu Arg His
 370 375 380
 Phe Asp Pro Glu Phe Thr Glu Glu Pro Val Pro Asn Ser Ile Gly Lys
 385 390 395 400
 Ser Pro Asp Ser Val Leu Val Thr Ala Ser Val Lys Glu Ala Ala Glu
 405 410 415
 Ala Phe Leu Gly Phe Ser Tyr Ala Pro Pro Thr Asp Ser Phe Leu
 420 425 430

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp	Pro	Glu	Phe	Thr	Glu	Glu	Pro	Val	Pro	Asn	Ser	Ile	Gly	Lys	Ser
1				5					10					15	

Pro Asp Ser

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu	Ala	Phe	Leu	Gly	Phe	Ser	Tyr	Ala	Pro	Pro	Thr	Asp	Ser	Phe	Leu
1				5					10					15	

10000039-120401